

#10/12/03



TECH CENTER 1600/2900

JAN 29 2003

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DATE: 01/23/2003

TIME: 08:02:08

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/710,339A

Input Set : A:\5835.ST25.txt

Output Set: N:\CRF4\01232003\I710339A.raw

3 <110> APPLICANT: Bisgard-Frantzen, Henrik  
 4 Pedersen, Sven  
 5 Svendsen, Allan  
 7 <120> TITLE OF INVENTION: Fungamyl-like Alpha-Amylase Variants  
 9 <130> FILE REFERENCE: 5835.200-US  
 11 <140> CURRENT APPLICATION NUMBER: US 09/710,339A  
 12 <141> CURRENT FILING DATE: 2000-11-09  
 14 <150> PRIOR APPLICATION NUMBER: US 60/165,786  
 15 <151> PRIOR FILING DATE: 1999-11-16  
 17 <160> NUMBER OF SEQ ID NOS: 6  
 19 <170> SOFTWARE: PatentIn version 3.1  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 1734  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Aspergillus Oryzae  
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 27 <221> NAME/KEY: CDS  
 28 <222> LOCATION: (54)..(1547)  
 29 <223> OTHER INFORMATION: mat\_peptide  
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 43 Val Ala Trp Trp Ser Leu Phe Leu Tyr Gly Leu Gln Val Ala Ala Pro  
 44 -15 -10 -5  
 46 gct ttg gct gca acg cct gcg gac tgg cga tcg caa tcc att tat ttc 152  
 47 Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe  
 48 -1 1 5 10  
 50 ctt ctc acg gat cga ttt gca agg acg gat ggg tcg acg act gcg act 200  
 51 Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr  
 52 15 20 25  
 54 tgt aat act gcg gat cag aaa tac tgt ggt gga aca tgg cag ggc atc 248  
 55 Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile  
 56 30 35 40 45  
 58 atc gac aag ttg gac tat atc cag gga atg ggc ttc aca gcc atc tgg 296  
 59 Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp  
 60 50 55 60  
 62 atc acc ccc gtt aca gcc cag ctg ccc cag acc acc gca tat gga gat 344

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66	gcc	tac	cat	ggc	tac	tgg	cag	cag	gat	ata	tac	tct	ctg	aac	gaa	aac	392
67	Ala	Tyr	His	Gly	Tyr	Trp	Gln	Gln	Asp	Ile	Tyr	Ser	Leu	Asn	Glu	Asn	
68			80				85						90				
70	tac	ggc	act	gca	gat	gac	ttg	aag	gcg	ctc	tct	tcg	gcc	ctt	cat	gag	440
71	Tyr	Gly	Thr	Ala	Asp	Asp	Leu	Lys	Ala	Leu	Ser	Ser	Ala	Leu	His	Glu	
72		95					100					105					
74	agg	ggg	atg	tat	ctt	atg	gtc	gat	gtg	gtt	gct	aac	cat	atg	ggc	tat	488
75	Arg	Gly	Met	Tyr	Leu	Met	Val	Asp	Val	Val	Ala	Asn	His	Met	Gly	Tyr	
76	110					115					120						
78	gat	gga	gcg	ggt	agc	tca	gtc	gat	tac	agt	gtg	ttt	aaa	ccg	ttc	agt	536
79	Asp	Gly	Ala	Gly	Ser	Ser	Val	Asp	Tyr	Ser	Val	Phe	Lys	Pro	Phe	Ser	
80				130					135					140			
82	tcc	caa	gac	tac	ttc	cac	ccg	ttc	tgt	ttc	att	caa	aac	tat	gaa	gat	584
83	Ser	Gln	Asp	Tyr	Phe	His	Pro	Phe	Cys	Phe	Ile	Gln	Asn	Tyr	Glu	Asp	
84			145						150				155				
86	cag	act	cag	gtt	gag	gat	tgc	tgg	cta	gga	gat	aac	act	gtc	tcc	ttg	632
87	Gln	Thr	Gln	Val	Glu	Asp	Cys	Trp	Leu	Gly	Asp	Asn	Thr	Val	Ser	Leu	
88			160				165					170					
90	cct	gat	ctc	gat	acc	acc	aag	gat	gtg	gtc	aag	aat	gaa	tgg	tac	gac	680
91	Pro	Asp	Leu	Asp	Thr	Thr	Lys	Asp	Val	Val	Lys	Asn	Glu	Trp	Tyr	Asp	
92		175					180				185						
94	tgg	gtg	gga	tca	ttg	gta	tcg	aac	tac	tcc	att	gac	ggc	ctc	cgt	atc	728
95	Trp	Val	Gly	Ser	Leu	Val	Ser	Asn	Tyr	Ser	Ile	Asp	Gly	Leu	Arg	Ile	
96	190				195				200				205				
98	gac	aca	gta	aaa	cac	gtc	cag	aag	gac	ttc	tgg	ccc	ggg	tac	aac	aaa	776
99	Asp	Thr	Val	Lys	His	Val	Gln	Lys	Asp	Phe	Trp	Pro	Gly	Tyr	Asn	Lys	
100			210						215				220				
102	gcc	gca	ggc	gtg	tac	tgt	atc	ggc	gag	gtg	ctc	gac	ggt	gat	ccg	gcc	824
103	Ala	Ala	Gly	Val	Tyr	Cys	Ile	Gly	Glu	Val	Leu	Asp	Gly	Asp	Pro	Ala	
104			225					230				235					
106	tac	act	tgt	ccc	tac	cag	aac	gtc	atg	gac	ggc	gta	ctg	aac	tat	ccc	872
107	Tyr	Thr	Cys	Pro	Tyr	Gln	Asn	Val	Met	Asp	Gly	Val	Leu	Asn	Tyr	Pro	
108			240				245				250						
110	att	tac	tat	cca	ctc	ctc	aac	gcc	ttc	aag	tca	acc	tcc	ggc	agc	atg	920
111	Ile	Tyr	Tyr	Pro	Leu	Leu	Asn	Ala	Phe	Lys	Ser	Thr	Ser	Gly	Ser	Met	
112		255				260				265							
114	gac	gac	ctc	tac	aac	atg	atc	aac	acc	gtc	aaa	tcc	gac	tgt	cca	gac	968
115	Asp	Asp	Leu	Tyr	Asn	Met	Ile	Asn	Thr	Val	Lys	Ser	Asp	Cys	Pro	Asp	
116	270				275				280				285				
118	tca	aca	ctc	ctg	ggc	aca	ttc	gtc	gag	aac	cac	gac	aac	cca	cgg	ttc	1016
119	Ser	Thr	Leu	Leu	Gly	Thr	Phe	Val	Glu	Asn	His	Asp	Asn	Pro	Arg	Phe	
120			290					295				300					
122	gct	tct	tac	acc	aac	gac	ata	gcc	ctc	gcc	aag	aac	gtc	gca	gca	ttc	1064
123	Ala	Ser	Tyr	Thr	Asn	Asp	Ile	Ala	Leu	Ala	Lys	Asn	Val	Ala	Ala	Phe	
124			305				310					315					
126	atc	atc	ctc	aac	gac	gga	atc	ccc	atc	tac	gcc	ggc	caa	gaa	cag		1112
127	Ile	Ile	Leu	Asn	Asp	Gly	Ile	Pro	Ile	Ile	Tyr	Ala	Gly	Gln	Glu	Gln	

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130 cac tac gcc ggc gga aac gac ccc gcg aac cgc gaa gca acc tgg ctc 1160
131 His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu
132          335          340          345
134 tcg ggc tac ccg acc gac agc gag ctg tac aag tta att gcc tcc gcg 1208
135 Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser Ala
136 350          355          360          365
138 aac gca atc cgg aac tat gcc att agc aaa gat aca gga ttc gtg acc 1256
139 Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val Thr
140          370          375          380
142 tac aag aac tgg ccc atc tac aaa gac gac aca acg atc gcc atg cgc 1304
143 Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met Arg
144          385          390          395
146 aag ggc aca gat ggg tcg cag atc gtg act atc ttg tcc aac aag ggt 1352
147 Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly
148          400          405          410
150 gct tcg ggt gat tcg tat acc ctc tcc ttg agt ggt gcg ggt tac aca 1400
151 Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr
152          415          420          425
154 gcc ggc cag caa ttg acg gag gtc att ggc tgc acg acc gtg acg gtt 1448
155 Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val
156 430          435          440          445
158 ggt tcg gat gga aat gtg cct gtt cct atg gca ggt ggg cta cct agg 1496
159 Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg
160          450          455          460
162 gta ttg tat ccg act gag aag ttg gca ggt agc aag atc tgt agt agc 1544
163 Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser Ser
164          465          470          475
166 tcg tgaagggtgg agagtatatg atggtactgc tattcaatct ggcattggac 1597
167 Ser
170 agtgagtttg agtttgatgt acagttggag tcgttactgc tgtcatcccc ttatactctt 1657
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189          -1 1          5          10
192 Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
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196 Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
197          30          35          40
200 Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
201 45          50          55          60
204 Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly

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212	Asn	Tyr	Gly	Thr	Ala	Asp	Asp	Leu	Lys	Ala	Leu	Ser	Ser	Ala
213			95					100					105	
216	Glu	Arg	Gly	Met	Tyr	Leu	Met	Val	Asp	Val	Val	Ala	Asn	His
217		110					115					120		
220	Tyr	Asp	Gly	Ala	Gly	Ser	Ser	Val	Asp	Tyr	Ser	Val	Phe	Lys
221	125					130					135			140
224	Ser	Ser	Gln	Asp	Tyr	Phe	His	Pro	Phe	Cys	Phe	Ile	Gln	Asn
225				145					150					155
228	Asp	Gln	Thr	Gln	Val	Glu	Asp	Cys	Trp	Leu	Gly	Asp	Asn	Thr
229			160					165					170	
232	Leu	Pro	Asp	Leu	Asp	Thr	Thr	Lys	Asp	Val	Val	Lys	Asn	Glu
233			175					180					185	
236	Asp	Trp	Val	Gly	Ser	Leu	Val	Ser	Asn	Tyr	Ser	Ile	Asp	Gly
237		190					195					200		
240	Ile	Asp	Thr	Val	Lys	His	Val	Gln	Lys	Asp	Phe	Trp	Pro	Gly
241	205					210					215			220
244	Lys	Ala	Ala	Gly	Val	Tyr	Cys	Ile	Gly	Glu	Val	Leu	Asp	Gly
245				225						230				235
248	Ala	Tyr	Thr	Cys	Pro	Tyr	Gln	Asn	Val	Met	Asp	Gly	Val	Leu
249			240						245				250	
252	Pro	Ile	Tyr	Tyr	Pro	Leu	Leu	Asn	Ala	Phe	Lys	Ser	Thr	Ser
253			255					260					265	
256	Met	Asp	Asp	Leu	Tyr	Asn	Met	Ile	Asn	Thr	Val	Lys	Ser	Asp
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260	Asp	Ser	Thr	Leu	Leu	Gly	Thr	Phe	Val	Glu	Asn	His	Asp	Asn
261	285				290					295				300
264	Phe	Ala	Ser	Tyr	Thr	Asn	Asp	Ile	Ala	Leu	Ala	Lys	Asn	Val
265				305						310				315
268	Phe	Ile	Ile	Leu	Asn	Asp	Gly	Ile	Pro	Ile	Ile	Tyr	Ala	Gly
269				320					325					330
272	Gln	His	Tyr	Ala	Gly	Gly	Asn	Asp	Pro	Ala	Asn	Arg	Glu	Ala
273			335					340					345	
276	Leu	Ser	Gly	Tyr	Pro	Thr	Asp	Ser	Glu	Leu	Tyr	Lys	Leu	Ile
277		350					355					360		
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281	365				370						375			380
284	Thr	Tyr	Lys	Asn	Trp	Pro	Ile	Tyr	Lys	Asp	Asp	Thr	Thr	Ile
285				385						390				395
288	Arg	Lys	Gly	Thr	Asp	Gly	Ser	Gln	Ile	Val	Thr	Ile	Leu	Ser
289			400					405					410	
292	Gly	Ala	Ser	Gly	Asp	Ser	Tyr	Thr	Leu	Ser	Leu	Ser	Gly	Ala
293			415					420					425	
296	Thr	Ala	Gly	Gln	Gln	Leu	Thr	Glu	Val	Ile	Gly	Cys	Thr	Thr
297		430					435					440		
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304 Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser
305                               465                               470                               475
308 Ser Ser
312 <210> SEQ ID NO: 3
313 <211> LENGTH: 498
314 <212> TYPE: PRT
315 <213> ORGANISM: Aspergillus oryzae
317 <400> SEQUENCE: 3
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324                               20                               25                               30
327 Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
328                               35                               40                               45
331 Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
332 50                               55                               60
335 Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
336 65                               70                               75                               80
339 Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
340                               85                               90                               95
343 Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
344                               100                              105                              110
347 Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
348                               115                              120                              125
351 Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
352 130                              135                              140
355 Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
356 145                              150                              155                              160
359 Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
360                               165                               170                               175
363 Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
364                               180                               185                               190
367 Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
368                               195                               200                               205
371 Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
372 210                              215                              220
375 Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
376 225                              230                              235                              240
379 Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
380                               245                               250                               255
383 Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
384                               260                               265                               270
387 Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
388                               275                               280                               285
391 Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
392 290                              295                              300
395 Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
396 305                              310                              315                              320
399 Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/710,339A

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